

Fig. 1A. ScFv library

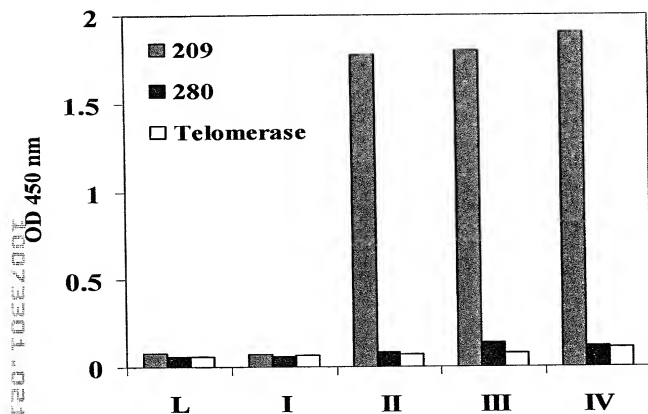


Fig. 1B. ScFv-CBD library

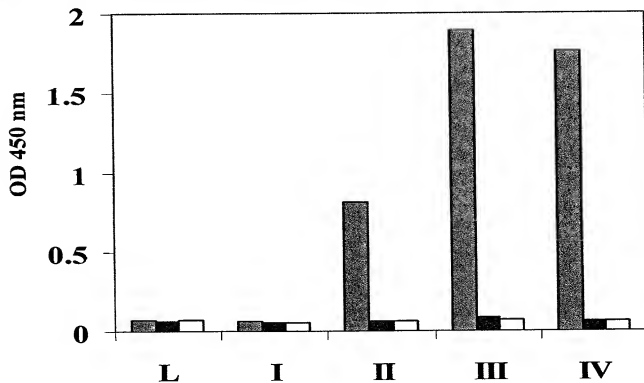


Fig. 2A. HLA-A2/G9-209

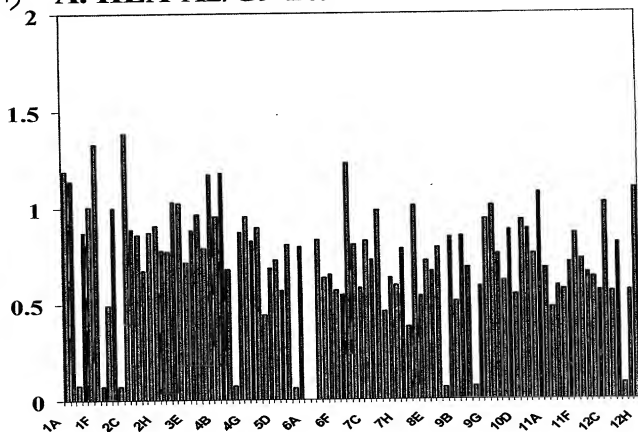


Fig. 2B. HLA-A2/G9-280

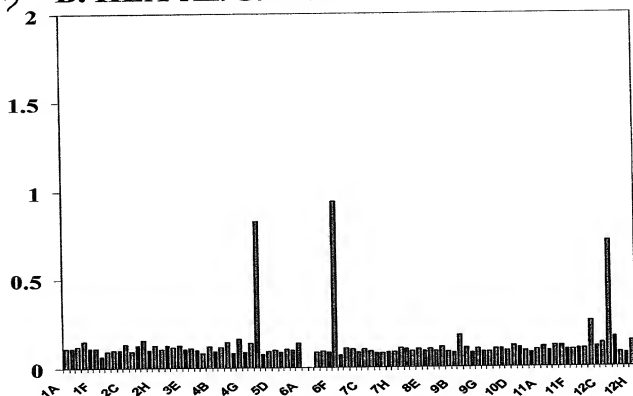


FIGURE 3A(i)

1 2 3 4 5 6 7 8 9 10 11 12 13 14
CAG GTG AAA CTG CAG GAG TCT GGG GGA GGC TTA GTG AAG CCT SEQ ID NO:8
gln val lys leu gln glu ser gly gly gly leu val lys pro SEQ ID NO:9

15 16 17 18 19 20 21 22 23 24 25 26 27 28
GGA GGG TCC CTG AAA CTC TCC TGT GCA GCC TCT GGA TTC ACT
gly gly ser leu lys leu ser cys ala ala ser gly phe thr

29 30 31 32 33 34 35 36 37 38 39 40 41 42
TTC AGT AGC TAT GGC ATG TCT TGG GTT CGC CAG ACT CCA GAC
phe ser ser tyr gly met ser trp val arg gln thr pro asp

43 44 45 46 47 48 49 50 51 52 53 54 55 56
AAG AGG CTG GAG TGG GTC GCA ACC ATT AGT AGT GGT GGT AGT
lys arg leu glu trp val ala thr ile ser ser gly gly ser

57 58 59 60 61 62 63 64 65 66 67 68 69 70
TAC ACC TAC TAT CCA GAC AGT GTG AAG GGG CGA TTC ACC ATC
tyr thr tyr tyr pro asp ser val lys gly arg phe thr ile

71 72 73 74 75 76 77 78 79 80 81 82 83 84
TCC AGA GAC AAT GCC AAG AAC ACC CTG TAC CTG CAA ATG AGC
ser arg asp asn ala lys asn thr leu tyr leu gln met ser

85 86 87 88 89 90 91 92 93 94 95 96 97 98
AGT CTG AAG TCT GAG GAC ACA GCC ATG TAT TAC TGT GCA AGA
ser leu lys ser glu asp thr ala met tyr tyr cys ala arg

99 100 101 102 103 104 105 106 107 108 109 110 111 112
GGT AAC TGG GAA GGA TGG TAC TTC GAT GTC TGG GGC CAA GGG
gly asn trp glu gly trp tyr phe asp val trp gly gln gly

113 114 115 116 117 118
ACC ACG GTC ACC GTC TCC TCA GGT GGA GGC GGT TCA GGC GGA
thr thr val thr val ser ser gly gly gly gly ser gly gly

1 2 3 4 5 6
GGT GGC TCT GGC GGT GGC GGA TCG AAC ATC GAG CTC ACT CAG
gly gly ser gly gly gly gly ser asn ile glu leu thr gln

7 8 9 10 11 12 13 14 15 16 17 18 19 20
TCT CCA GCA ATC ATG TCT GCA TCT CCA GGG GAG AGG GTC ACC
ser pro ala ile met ser ala ser pro gly glu arg val thr

21 22 23 24 25 26 27 28 29 30 31 32 33 34
ATG ACC TGC AGT GCC AGC TCA AGT ATA CGT TAC ATA TAT TGG
met thr cys ser ala ser ser ser ile arg tyr ile tyr trp

35 36 37 38 39 40 41 42 43 44 45 46 47 48
TAC CAA CAG AAG CCT GGA TCC TCC CCC AGA CTC CTG ATT TAT
tyr gln gln lys pro gly ser ser pro arg leu leu ile tyr

49 50 51 52 53 54 55 56 57 58 59 60 61 62
GAC ACA TCC AAC GTG GCT CCT GGA GTC CCT TTT CGC TTC AGT
asp thr ser asn val ala pro gly val pro phe arg phe ser

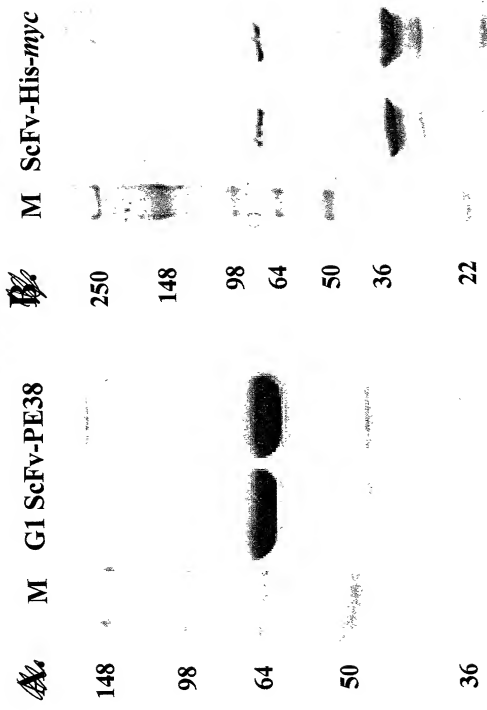
FIGURE 3A(ii)

63 64 65 66 67 68 69 70 71 72 73 74 75 76
GGC AGT GGG TCT GGG ACC TCT TAT TCT CTC ACA ATC AAC CGA
gly ser gly ser gly thr ser tyr ser leu thr ile asn arg

77 78 79 80 81 82 83 84 85 86 87 88 89 90
ATG GAG GCT GAG GAT GCT GCC ACT TAT TAC TGC CAG GAG TGG
met glu ala glu asp ala ala thr tyr tyr cys gln glu trp

91 92 93 94 95 96 97 98 99 100 101 102 103
AGT GGT TAT CCG TAC ACG TTC GGA GGG GGG ACA AAG TTG
ser gly tyr pro tyr thr phe gly gly gly thr lys leu

1473301-024302



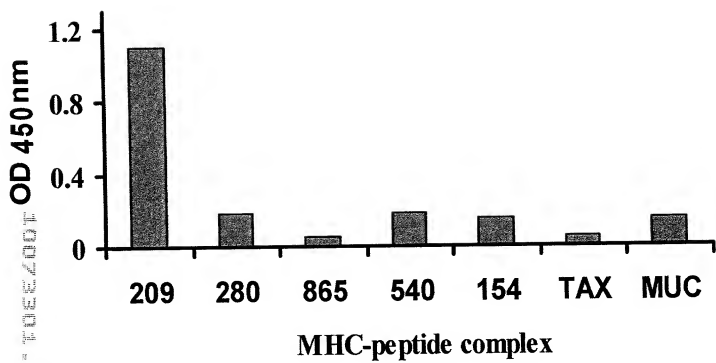


Fig. 4

Fig. 5A

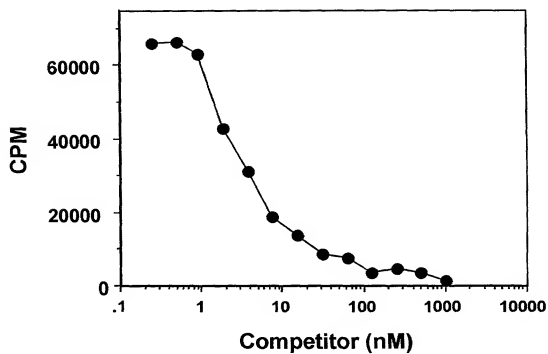
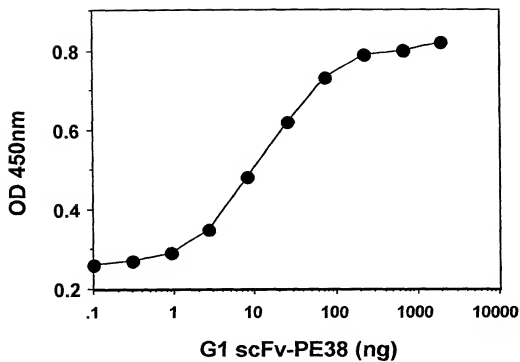
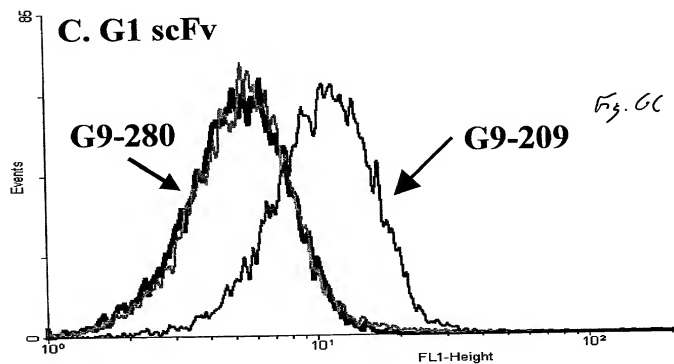
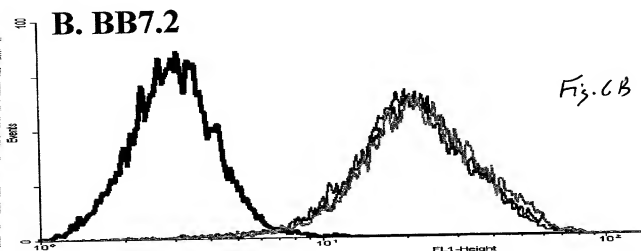
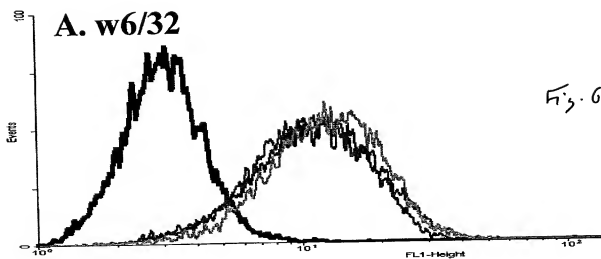


Fig. 5B



Protein synthesis (% of control)

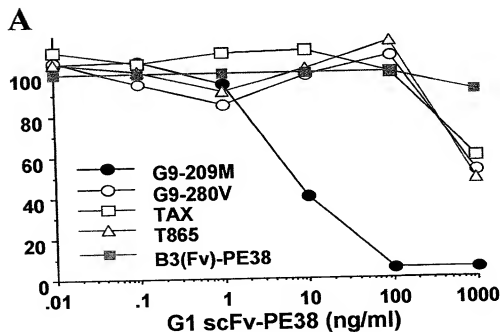


Fig. 7A

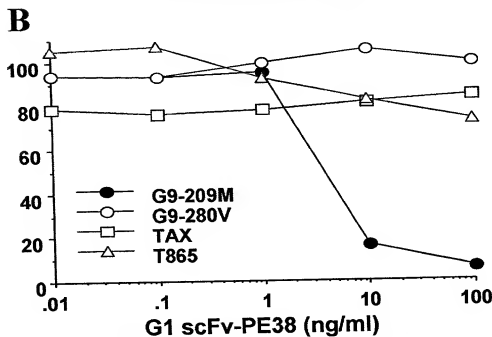


Fig. 7B

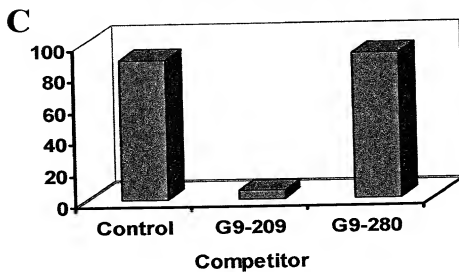


Fig. 7C